



SEQUENCE LISTING

<110> Merck & Co., Inc.

LaMonica, Nicola

Facciabene, Andrea

Aurisicchio, Luigi

<120> CARCINOEMBRYONIC ANTIGEN FUSIONS AND

USES THEREOF

<130> ITR0073YP

<140> 10/589,180

<141> 2006-08-11

<150> PCT/EP2005/001114

<151> 2005-02-03

<150> 60/635,791

<151> 2004-12-14

<150> 60/543,649

<151> 2004-02-11

<160> 54

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<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

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<223> PCR Primer, chemically synthesized

<400> 2
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<210> 3
<211> 35
<212> DNA
<213> Artificial Sequence

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<223> PCR Primer, chemically synthesized

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<210> 4
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<212> DNA
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<223> CEA-LTA fusion

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catctttttg gctacagctg gtacaaaggt gaaagagtgg atggcaaccg tcaaattata 240
ggatatgtaa taggaactca acaagctacc ccagggccccg catacagtgg tcgagagata 300
atatacccca atgcatccct gctgatccag aacatcatcc agaatgacac aggattctac 360

accctacacg tcataaagtc agatcttgtg aatgaagaag caactggcca gttccggta 420
 taccggagc tgcccaagcc ctccatctcc agcaacaact ccaaaccgt ggaggacaag 480
 gatgctgtgg cttcacctg tgaacctgag actcaggacg caacctacct gtggtggta 540
 aacaatcaga gcctcccggt cagtcacagg ctgcagctgt ccaatggcaa caggaccctc 600
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 gagccaccca aacccttcat caccagcaac aactccaacc ccgtggagga tgaggatgct 1020
 gtagccttaa cctgtgaacc tgagattcag aacacaacct acctgtggta ggtaaataat 1080
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 aactcagcca gtggccacag caggactaca gtcaagacaa tcacagtctc tgccggagctg 1500
 cccaagccct ccatctccag caacaactcc aaacccgtgg aggacaagga tgctgtggcc 1560
 ttcacctgtg aacctgaggc tcagaacaca acctacctgt ggtggtaaa tggtcagagc 1620
 ctcccagtca gtcccaggct gcagctgtcc aatggcaaca ggaccctcac tctattcaat 1680
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<210> 8
 <211> 921
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CEA-LTB fusion

<400> 8

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Thr	Ala	Lys	Leu	Thr	Ile	Glu	Ser	Thr	Pro	Phe	Asn	Val	Ala	Glu	Gly
35															
Lys	Glu	Val	Leu	Leu	Leu	Val	His	Asn	Leu	Pro	Gln	His	Leu	Phe	Gly
50															
Tyr	Ser	Trp	Tyr	Lys	Gly	Glu	Arg	Val	Asp	Gly	Asn	Arg	Gln	Ile	Ile
65															
Gly	Tyr	Val	Ile	Gly	Thr	Gln	Gln	Ala	Thr	Pro	Gly	Pro	Ala	Tyr	Ser
85															
Gly	Arg	Glu	Ile	Ile	Tyr	Pro	Asn	Ala	Ser	Leu	Leu	Ile	Gln	Asn	Ile
100															
Ile	Gln	Asn	Asp	Thr	Gly	Phe	Tyr	Thr	Leu	His	Val	Ile	Lys	Ser	Asp
115															
Leu	Val	Asn	Glu	Glu	Ala	Thr	Gly	Gln	Phe	Arg	Val	Tyr	Pro	Glu	Leu
130															
Pro	Lys	Pro	Ser	Ile	Ser	Ser	Asn	Asn	Ser	Lys	Pro	Val	Glu	Asp	Lys
145															
Asp	Ala	Val	Ala	Phe	Thr	Cys	Glu	Pro	Glu	Thr	Gln	Asp	Ala	Thr	Tyr
165															
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180	185	190
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195	200	205
Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg		
210	215	220
Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro		
225	230	235
Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn		
245	250	255
Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe		
260	265	270
Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn		
275	280	285
Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser		
290	295	300
Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala		
305	310	315
Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu		
325	330	335
Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr		
340	345	350
Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg		
355	360	365
Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr		
370	375	380
Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser		
385	390	395
Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp		
405	410	415
Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn		
420	425	430
Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser		
435	440	445
Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile		
450	455	460
Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn		
465	470	475
480		

Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val
 485 490 495
 Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro
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 Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln
 515 520 525
 Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser
 530 535 540
 Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn
 545 550 555 560
 Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser
 565 570 575
 Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly
 580 585 590
 Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly
 595 600 605
 Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln
 610 615 620
 Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
 625 630 635 640
 Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
 645 650 655
 Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile
 660 665 670
 Thr Val Ser Ala Ser Gly Thr Leu Val Asn Gly Asp Lys Leu Tyr Arg
 675 680 685
 Ala Asp Ser Arg Pro Pro Asp Glu Ile Lys Arg Ser Gly Gly Leu Met
 690 695 700
 Pro Arg Gly His Asn Glu Tyr Phe Asp Arg Gly Thr Gln Met Asn Ile
 705 710 715 720
 Asn Leu Tyr Asp His Ala Arg Gly Thr Gln Thr Gly Phe Val Arg Tyr
 725 730 735
 Asp Asp Gly Tyr Val Ser Thr Ser Leu Ser Leu Arg Ser Ala His Leu
 740 745 750
 Ala Gly Gln Ser Ile Leu Ser Gly Tyr Ser Thr Tyr Tyr Ile Tyr Val
 755 760 765
 Ile Ala Thr Ala Pro Asn Met Phe Asn Val Asn Asp Val Leu Gly Val

770	775	780
Tyr Ser Pro His Pro Tyr Glu Gln Glu Val Ser Ala Leu Gly Gly Ile		
785	790	795
Pro Tyr Ser Gln Ile Tyr Gly Trp Tyr Arg Val Asn Phe Gly Val Ile		800
805	810	815
Asp Glu Arg Leu His Arg Asn Arg Glu Tyr Arg Asp Arg Tyr Tyr Arg		
820	825	830
Asn Leu Asn Ile Ala Pro Ala Glu Asp Gly Tyr Arg Leu Ala Gly Phe		
835	840	845
Pro Pro Asp His Gln Ala Trp Arg Glu Glu Pro Trp Ile His His Ala		
850	855	860
Pro Gln Gly Cys Gly Asn Ser Ser Arg Thr Ile Thr Asp Asp Thr Cys		
865	870	875
Asn Glu Glu Thr Gln Asn Leu Ser Thr Ile Tyr Leu Arg Lys Tyr Gln		
885	890	895
Ser Lys Val Lys Arg Gln Ile Phe Ser Asp Tyr Gln Ser Glu Val Asp		
900	905	910
Ile Tyr Asn Arg Ile Arg Asp Glu Leu		
915	920	

<210> 9
 <211> 2355
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CEA-LTB fusion

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<210> 10

<211> 784

<212> PRT

<213> Artificial Sequence

<220>

<223> CEA-LTB fusion

<400> 10

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Thr	Ala	Lys	Leu	Thr	Ile	Glu	Ser	Thr	Pro	Phe	Asn	Val	Ala	Glu	Gly
		35				40						45			
Lys	Glu	Val	Leu	Leu	Val	His	Asn	Leu	Pro	Gln	His	Leu	Phe	Gly	
	50				55			60							
Tyr	Ser	Trp	Tyr	Lys	Gly	Glu	Arg	Val	Asp	Gly	Asn	Arg	Gln	Ile	Ile
65			70					75					80		
Gly	Tyr	Val	Ile	Gly	Thr	Gln	Gln	Ala	Thr	Pro	Gly	Pro	Ala	Tyr	Ser
		85				90						95			
Gly	Arg	Glu	Ile	Ile	Tyr	Pro	Asn	Ala	Ser	Leu	Leu	Ile	Gln	Asn	Ile
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Ile	Gln	Asn	Asp	Thr	Gly	Phe	Tyr	Thr	Leu	His	Val	Ile	Lys	Ser	Asp
		115				120					125				
Leu	Val	Asn	Glu	Glu	Ala	Thr	Gly	Gln	Phe	Arg	Val	Tyr	Pro	Glu	Leu
	130				135			140							
Pro	Lys	Pro	Ser	Ile	Ser	Ser	Asn	Asn	Ser	Lys	Pro	Val	Glu	Asp	Lys
145					150			155				160			
Asp	Ala	Val	Ala	Phe	Thr	Cys	Glu	Pro	Glu	Thr	Gln	Asp	Ala	Thr	Tyr
		165				170					175				
Leu	Trp	Trp	Val	Asn	Asn	Gln	Ser	Leu	Pro	Val	Ser	Pro	Arg	Leu	Gln
		180				185					190				
Leu	Ser	Asn	Gly	Asn	Arg	Thr	Leu	Thr	Leu	Phe	Asn	Val	Thr	Arg	Asn
		195				200					205				
Asp	Thr	Ala	Ser	Tyr	Lys	Cys	Glu	Thr	Gln	Asn	Pro	Val	Ser	Ala	Arg
210				215					220						
Arg	Ser	Asp	Ser	Val	Ile	Leu	Asn	Val	Leu	Tyr	Gly	Pro	Asp	Ala	Pro
225				230				235					240		
Thr	Ile	Ser	Pro	Leu	Asn	Thr	Ser	Tyr	Arg	Ser	Gly	Glu	Asn	Leu	Asn

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Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe		
260	265	270
Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn		
275	280	285
Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser		
290	295	300
Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala		
305	310	315
Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu		
325	330	335
Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr		
340	345	350
Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg		
355	360	365
Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr		
370	375	380
Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser		
385	390	395
Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp		
405	410	415
Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn		
420	425	430
Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser		
435	440	445
Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile		
450	455	460
Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn		
465	470	475
Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val		
485	490	495
Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro		
500	505	510
Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln		
515	520	525
Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser		
530	535	540

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 Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser
 565 570 575
 Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly
 580 585 590
 Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly
 595 600 605
 Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln
 610 615 620
 Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
 625 630 635 640
 Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
 645 650 655
 Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile
 660 665 670
 Thr Val Ser Ala Ser Gly Thr Leu Asp Ala Pro Gln Ser Ile Thr Glu
 675 680 685
 Leu Cys Ser Glu Tyr Arg Asn Thr Gln Ile Tyr Thr Ile Asn Asp Lys
 690 695 700
 Ile Leu Ser Tyr Thr Glu Ser Met Ala Gly Lys Arg Glu Met Val Ile
 705 710 715 720
 Ile Thr Phe Lys Ser Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser
 725 730 735
 Gln His Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr
 740 745 750
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 755 760 765
 Trp Asn Asn Lys Thr Pro Asn Ser Ile Ala Ala Ile Ser Met Glu Asn
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<210> 11
 <211> 2355
 <212> DNA
 <213> Artificial Sequence

<220>

<223> CEAopt-LTB fusion

<400> 11

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<210> 12
 <211> 2358
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CEAopt-LTBopt fusion

<400> 12

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 acccccttca acgtggccga gggcaaggag gtgctgctgc tggtgcacaa cctgccccag 180
 cacctgttcg gctacagctg gtacaaggagc gagcgcgtgg acggcaacccg ccagatcatc 240
 ggctacgtga tcggcaccca gcaggccacc cccggccccc cctacagcgg ccgcgagatc 300
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 aacaaccaga gcctgcccgt gagccccccgc ctgcagctga gcaacggcaa ccgcaccctg 600
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 gtgagcgccc gccgcagcga cagcgtgatc ctgaacgtgc tgtacggccc cgacgcccc 720
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<210> 13

<211> 784

<212> PRT

<213> Artificial Sequence

<220>

<223> CEAopt-LTBopt fusion

<400> 13

Met	Glu	Ser	Pro	Ser	Ala	Pro	Pro	His	Arg	Trp	Cys	Ile	Pro	Trp	Gln
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Arg	Leu	Leu	Leu	Thr	Ala	Ser	Leu	Leu	Thr	Phe	Trp	Asn	Pro	Pro	Thr
20								25						30	

Thr	Ala	Lys	Leu	Thr	Ile	Glu	Ser	Thr	Pro	Phe	Asn	Val	Ala	Glu	Gly
35								40						45	

Lys	Glu	Val	Leu	Leu	Val	His	Asn	Leu	Pro	Gln	His	Leu	Phe	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50	55	60	
Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile			
65	70	75	80
Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser			
85	90		95
Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile			
100	105	110	
Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp			
115	120	125	
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu			
130	135	140	
Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys			
145	150	155	160
Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr			
165	170	175	
Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln			
180	185	190	
Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn			
195	200	205	
Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg			
210	215	220	
Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro			
225	230	235	240
Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn			
245	250	255	
Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe			
260	265	270	
Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn			
275	280	285	
Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser			
290	295	300	
Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala			
305	310	315	320
Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu			
325	330	335	
Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr			
340	345	350	

Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
 355 360 365
 Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr
 370 375 380
 Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser
 385 390 395 400
 Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp
 405 410 415
 Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn
 420 425 430
 Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser
 435 440 445
 Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
 450 455 460
 Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn
 465 470 475 480
 Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val
 485 490 495
 Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro
 500 505 510
 Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln
 515 520 525
 Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser
 530 535 540
 Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn
 545 550 555 560
 Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser
 565 570 575
 Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly
 580 585 590
 Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly
 595 600 605
 Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln
 610 615 620
 Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
 625 630 635 640
 Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe

645	650	655
Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile		
660	665	670
Thr Val Ser Ala Ser Gly Thr Ser Arg Ala Pro Gln Ser Ile Thr Glu		
675	680	685
Leu Cys Ser Glu Tyr Arg Asn Thr Gln Ile Tyr Thr Ile Asn Asp Lys		
690	695	700
Ile Leu Ser Tyr Thr Glu Ser Met Ala Gly Lys Arg Glu Met Val Ile		
705	710	715
Ile Thr Phe Lys Ser Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser		
725	730	735
Gln His Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr		
740	745	750
Leu Arg Ile Thr Tyr Leu Thr Glu Thr Lys Ile Asp Lys Leu Cys Val		
755	760	765
Trp Asn Asn Lys Thr Pro Asn Ser Ile Ala Ala Ile Ser Met Glu Asn		
770	775	780

<210> 14
 <211> 2358
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> rhCEAopt-LTBopt fusion

<400> 14
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 cggcccttca acgtggccga gggcaaggag gtgctgctgc tggcccacaa cgtgagccag 180
 aacctgttcg gctacatctg gtacaagggc gagcgcgtgg acgccagccg ccgcacatccgc 240
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aacaaccaga gcctgcccgt gagcccccgc ctggagctga gcagcgacaa ccgcaccctg 600
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2358

<210> 15
 <211> 784
 <212> PRT
 <213> Artificial Sequence

<220>

<223> rhCEAopt-LTBopt fusion

<400> 15

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 20 25 30
 Thr Ala Gln Leu Thr Ile Glu Ser Arg Pro Phe Asn Val Ala Glu Gly
 35 40 45
 Lys Glu Val Leu Leu Ala His Asn Val Ser Gln Asn Leu Phe Gly
 50 55 60
 Tyr Ile Trp Tyr Lys Gly Glu Arg Val Asp Ala Ser Arg Arg Ile Gly
 65 70 75 80
 Ser Cys Val Ile Arg Thr Gln Gln Ile Thr Pro Gly Pro Ala His Ser
 85 90 95
 Gly Arg Glu Thr Ile Asp Phe Asn Ala Ser Leu Leu Ile His Asn Val
 100 105 110
 Thr Gln Ser Asp Thr Gly Ser Tyr Thr Ile Gln Val Ile Lys Glu Asp
 115 120 125
 Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
 130 135 140
 Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys
 145 150 155 160
 Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr Thr Tyr
 165 170 175
 Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Glu
 180 185 190
 Leu Ser Ser Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro Arg Asn
 195 200 205
 Asp Thr Thr Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Val Arg
 210 215 220
 Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
 225 230 235 240
 Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn Leu Asn
 245 250 255
 Leu Thr Cys His Ala Ala Ser Asn Pro Thr Ala Gln Tyr Phe Trp Phe

260	265	270
Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn		
275	280	285
Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His Asn Ser		
290	295	300
Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val Tyr Ala		
305	310	315
Glu Leu Pro Lys Pro Tyr Ile Thr Ser Asn Asn Ser Asn Pro Ile Glu		
325	330	335
Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr		
340	345	350
Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser Ser Arg		
355	360	365
Leu Glu Leu Ser Asn Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro		
370	375	380
Arg Asn Asp Thr Thr Phe Tyr Glu Cys Glu Thr Gln Asn Pro Val Ser		
385	390	395
Val Arg Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp		
405	410	415
Ala Pro Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn		
420	425	430
Leu Asn Leu Ser Cys His Ala Ala Ser Asn Pro Ala Ala Gln Tyr Ser		
435	440	445
Trp Phe Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile		
450	455	460
Pro Asn Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His		
465	470	475
Asn Ser Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val		
485	490	495
Tyr Val Glu Leu Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro		
500	505	510
Ile Glu Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Val Ala Glu		
515	520	525
Asn Thr Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser		
530	535	540
Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Ile Leu Thr Leu Leu Ser		
545	550	555
		560

Val Thr Arg Asn Asp Thr Gly Pro Tyr Glu Cys Gly Ile Gln Asn Ser
 565 570 575
 Glu Ser Ala Lys Arg Ser Asp Pro Val Thr Leu Asn Val Thr Tyr Gly
 580 585 590
 Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Leu Ser Tyr Arg Ser Gly
 595 600 605
 Ala Asn Leu Asn Leu Ser Cys His Ser Asp Ser Asn Pro Ser Pro Gln
 610 615 620
 Tyr Ser Trp Leu Ile Asn Gly Thr Leu Arg Gln His Thr Gln Val Leu
 625 630 635 640
 Phe Ile Ser Lys Ile Thr Ser Asn Asn Ser Gly Ala Tyr Ala Cys Phe
 645 650 655
 Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Asn Ile
 660 665 670
 Ser Val Ser Ser Gly Asp Ser Ser Arg Ala Pro Gln Ser Ile Thr Glu
 675 680 685
 Leu Cys Ser Glu Tyr Arg Asn Thr Gln Ile Tyr Thr Ile Asn Asp Lys
 690 695 700
 Ile Leu Ser Tyr Thr Glu Ser Met Ala Gly Lys Arg Glu Met Val Ile
 705 710 715 720
 Ile Thr Phe Lys Ser Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser
 725 730 735
 Gln His Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr
 740 745 750
 Leu Arg Ile Thr Tyr Leu Thr Glu Thr Lys Ile Asp Lys Leu Cys Val
 755 760 765
 Trp Asn Asn Lys Thr Pro Asn Ser Ile Ala Ala Ile Ser Met Glu Asn
 770 775 780

<210> 16
 <211> 2118
 <212> DNA
 <213> Macaca mulatta

<400> 16
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 aggccgttca atgttgcaga ggggaaggag gttcttctac ttgcccacaa tgtgtcccag 180
 aatcttttg gctacatttg gtacaaggga gaaagagtgg atgccagccg tcgaattgga 240
 tcatgtgtaa taagaactca acaaattacc ccagggcccg cacacagcgg tcgagagaca 300
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 accatacaag tcataaagga agatcttgc aatgaagaag caactggcca gttccggta 420
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 aacaatcaga gcctcccggt cagtcccagg ctggagctgt ccagtgacaa caggaccctc 600
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2118

<211> 2118
 <212> DNA
 <213> Macaca mulatta

<400> 17

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<210> 18

<211> 705

<212> PRT

<213> Macaca mulatta

<400> 18

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Thr Ala Gln Leu Thr Ile Glu Ser Arg Pro Phe Asn Val Ala Glu Gly

35 40 45

Lys Glu Val Leu Leu Leu Ala His Asn Val Ser Gln Asn Leu Phe Gly

50 55 60

Tyr Ile Trp Tyr Lys Gly Glu Arg Val Asp Ala Ser Arg Arg Ile Gly

65 70 75 80

Ser Cys Val Ile Arg Thr Gln Gln Ile Thr Pro Gly Pro Ala His Ser

85 90 95

Gly Arg Glu Thr Ile Asp Phe Asn Ala Ser Leu Leu Ile His Asn Val

100 105 110

Thr Gln Ser Asp Thr Gly Ser Tyr Thr Ile Gln Val Ile Lys Glu Asp

115 120 125

Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu

130 135 140

Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys

145 150 155 160

Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr Thr Tyr

165 170 175

Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Glu

180 185 190

Leu Ser Ser Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro Arg Asn

195 200 205

Asp Thr Thr Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Val Arg
 210 215 220
 Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
 225 230 235 240
 Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn Leu Asn
 245 250 255
 Leu Thr Cys His Ala Ala Ser Asn Pro Thr Ala Gln Tyr Phe Trp Phe
 260 265 270
 Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
 275 280 285
 Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His Asn Ser
 290 295 300
 Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val Tyr Ala
 305 310 315 320
 Glu Leu Pro Lys Pro Tyr Ile Thr Ser Asn Asn Ser Asn Pro Ile Glu
 325 330 335
 Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr
 340 345 350
 Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser Ser Arg
 355 360 365
 Leu Glu Leu Ser Asn Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro
 370 375 380
 Arg Asn Asp Thr Thr Phe Tyr Glu Cys Glu Thr Gln Asn Pro Val Ser
 385 390 395 400
 Val Arg Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp
 405 410 415
 Ala Pro Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn
 420 425 430
 Leu Asn Leu Ser Cys His Ala Ala Ser Asn Pro Ala Ala Gln Tyr Ser
 435 440 445
 Trp Phe Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile
 450 455 460
 Pro Asn Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His
 465 470 475 480
 Asn Ser Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val
 485 490 495
 Tyr Val Glu Leu Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro

500	505	510
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515	520	525
Asn Thr Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser		
530	535	540
Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Ile Leu Thr Leu Leu Ser		
545	550	555
560		
Val Thr Arg Asn Asp Thr Gly Pro Tyr Glu Cys Gly Ile Gln Asn Ser		
565	570	575
Glu Ser Ala Lys Arg Ser Asp Pro Val Thr Leu Asn Val Thr Tyr Gly		
580	585	590
Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Leu Ser Tyr Arg Ser Gly		
595	600	605
Ala Asn Leu Asn Leu Ser Cys His Ser Asp Ser Asn Pro Ser Pro Gln		
610	615	620
Tyr Ser Trp Leu Ile Asn Gly Thr Leu Arg Gln His Thr Gln Val Leu		
625	630	635
640		
Phe Ile Ser Lys Ile Thr Ser Asn Asn Ser Gly Ala Tyr Ala Cys Phe		
645	650	655
Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Asn Ile		
660	665	670
Ser Val Ser Ser Gly Asp Ser Ala Pro Gly Ser Ser Gly Leu Ser Ala		
675	680	685
Arg Ala Thr Val Gly Ile Ile Gly Met Leu Val Gly Val Ala Leu		
690	695	700
Met		
705		

<210> 19
 <211> 705
 <212> PRT
 <213> Macaca mulatta

<400> 19
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 Thr Ala Gln Leu Thr Ile Glu Ser Arg Pro Phe Asn Val Ala Glu Gly
 35 40 45
 Lys Glu Val Leu Leu Ala His Asn Val Ser Gln Asn Leu Phe Gly
 50 55 60
 Tyr Ile Trp Tyr Lys Gly Glu Arg Val Asp Ala Ser Arg Arg Ile Gly
 65 70 75 80
 Ser Cys Val Ile Arg Thr Gln Gln Ile Thr Pro Gly Pro Ala His Ser
 85 90 95
 Gly Arg Glu Thr Ile Asp Phe Asn Ala Ser Leu Leu Ile His Asn Val
 100 105 110
 Thr Gln Ser Asp Thr Gly Ser Tyr Thr Ile Gln Val Ile Lys Glu Asp
 115 120 125
 Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
 130 135 140
 Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys
 145 150 155 160
 Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr Thr Tyr
 165 170 175
 Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Glu
 180 185 190
 Leu Ser Ser Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro Arg Asn
 195 200 205
 Asp Thr Thr Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Val Arg
 210 215 220
 Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
 225 230 235 240
 Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn Leu Asn
 245 250 255
 Leu Thr Cys His Ala Ala Ser Asn Pro Thr Ala Gln Tyr Phe Trp Phe
 260 265 270
 Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
 275 280 285
 Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His Asn Ser
 290 295 300
 Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val Tyr Ala

305	310	315	320
Glu Leu Pro Lys Pro Tyr Ile Thr Ser Asn Asn Ser Asn Pro Ile Glu			
325	330	335	
Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr			
340	345	350	
Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser Ser Arg			
355	360	365	
Leu Glu Leu Ser Asn Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro			
370	375	380	
Arg Asn Asp Thr Thr Phe Tyr Glu Cys Glu Thr Gln Asn Pro Val Ser			
385	390	395	400
Val Arg Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp			
405	410	415	
Ala Pro Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn			
420	425	430	
Leu Asn Leu Ser Cys His Ala Ala Ser Asn Pro Ala Ala Gln Tyr Phe			
435	440	445	
Trp Phe Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile			
450	455	460	
Pro Asn Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His			
465	470	475	480
Asn Ser Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val			
485	490	495	
Tyr Val Glu Leu Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro			
500	505	510	
Ile Glu Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Val Ala Glu			
515	520	525	
Asn Thr Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser			
530	535	540	
Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Ile Leu Thr Leu Leu Ser			
545	550	555	560
Val Thr Arg Asn Asp Thr Gly Pro Tyr Glu Cys Gly Ile Gln Asn Ser			
565	570	575	
Glu Ser Ala Lys Arg Ser Asp Pro Val Thr Leu Asn Val Thr Tyr Gly			
580	585	590	
Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Leu Ser Tyr Arg Ser Gly			
595	600	605	

Ala Asn Leu Asn Leu Ser Cys His Ser Asp Ser Asn Pro Ser Pro Gln
 610 615 620
 Tyr Ser Trp Leu Ile Asn Gly Thr Leu Arg Gln His Thr Gln Val Leu
 625 630 635 640
 Phe Ile Ser Lys Ile Thr Ser Asn Asn Asn Gly Ala Tyr Ala Cys Phe
 645 650 655
 Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Asn Ile
 660 665 670
 Ser Val Ser Ser Gly Asp Ser Ala Pro Gly Ser Ser Gly Leu Ser Ala
 675 680 685
 Arg Ala Thr Val Gly Ile Ile Gly Met Leu Val Gly Val Ala Leu
 690 695 700
 Met
 705

<210> 20
 <211> 702
 <212> PRT
 <213> Homo sapiens

<400> 20
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 Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
 35 40 45
 Lys Glu Val Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
 50 55 60
 Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
 65 70 75 80
 Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
 85 90 95
 Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
 100 105 110
 Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp

115	120	125
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu		
130	135	140
Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys		
145	150	155
Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr		
165	170	175
Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln		
180	185	190
Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn		
195	200	205
Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg		
210	215	220
Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro		
225	230	235
Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn		
245	250	255
Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe		
260	265	270
Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn		
275	280	285
Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser		
290	295	300
Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala		
305	310	315
Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu		
325	330	335
Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr		
340	345	350
Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg		
355	360	365
Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr		
370	375	380
Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser		
385	390	395
Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp		
405	410	415

Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn
 420 425 430
 Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser
 435 440 445
 Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
 450 455 460
 Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn
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 485 490 495
 Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro
 500 505 510
 Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln
 515 520 525
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 530 535 540
 Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn
 545 550 555 560
 Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser
 565 570 575
 Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly
 580 585 590
 Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly
 595 600 605
 Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln
 610 615 620
 Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
 625 630 635 640
 Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
 645 650 655
 Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile
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<212> DNA
<213> Artificial Sequence

<220>
<223> CEAoptDOMopt fusion

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<210> 22

<211> 2037

<212> DNA

<213> Artificial Sequence

<220>

<223> deleted human CEA

<400> 22

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<210> 28

<211> 3585

<212> DNA

<213> Artificial Sequence

<220>

<223> CEA-VSVG fusion

<400> 28

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ggatatgtaa taggaactca acaagctacc ccagggcccg catacagtgg tcgagagata 300
atatacccca atgcatccct gctgatccag aacatcatcc agaatgacac aggattctac 360
accctacacg tcataaaagtc agatcttgcg aatgaagaag caactggcca gttccgggta 420
tacccggagc tgcccaagcc ctccatctcc agcaacaact ccaaaccgt ggaggacaag 480
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aacaatcaga gcctcccggt cagtcacccagg ctgcagctgt ccaatggcaa caggaccctc 600
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 ctattcttgg ttctccgagt tggatatttca ttttacattaa aattaaagca caccaagaaa 3540
 agacagattt atacagacat agagatgaac cgacttggaa ggtaa 3585

<210> 29

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

<400> 29

tattctagat tcaacaccaa ttccatttc ttattc

36

<210> 30

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

<400> 30

gcggccgcta gaatcatttg tccatccttc atc

33

<210> 31

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

<400> 31

tattctagat tcaacaccaa ttccatttc ttattc

36

<210> 32

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

<400> 32

ttagcggccg ctagttctgt atcatatcgt aaaggg

36

<210> 33

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

<400> 33

tcttagataaa actcacacat gccca

25

<210> 34

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

<400> 34

gccgactcat ttacccggag acagggag

28

<210> 35

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

<400> 35

tcttagatttg atccccattg ctgtgggcgg tgccctg

37

<210> 36

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

<400> 36

ggcgtgactc ctcttcctgc caatgaggta ggcaatgag

39

<210> 37

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

<400> 37

atatcttagat ttcaccatag ttttccaca caacc

35

<210> 38

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

<400> 38

gcggccgcct tccttccaag tcggttcatc tctatg

36

<210> 39

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

<400> 39

gctctagata tggctcgtgc ggtcggtatc gacc

34

<210> 40

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

<400> 40

gccgcggccg ctcacttggc ctcccgcccg tcgtcg

36

<210> 41

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

<400> 41

gttatctaga agcaccccca tccc

24

<210> 42

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

<400> 42
ttaagatctc taagatctgg tgtcgtatct cagggg 36

<210> 43
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer, chemically synthesized

<400> 43
ttatctagaa agaccacac ctgccccct tgc 33

<210> 44
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer, chemically synthesized

<400> 44
tatacatctt agggtacctt acttgccggg g 31

<210> 45
<211> 952
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA-Dom fusion

<400> 45
Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile Pro Trp Gln
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Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
 20 25 30
 Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
 35 40 45
 Lys Glu Val Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
 50 55 60
 Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
 65 70 75 80
 Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
 85 90 95
 Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
 100 105 110
 Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
 115 120 125
 Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
 130 135 140
 Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
 145 150 155 160
 Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
 165 170 175
 Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
 180 185 190
 Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
 195 200 205
 Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
 210 215 220
 Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
 225 230 235 240
 Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
 245 250 255
 Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
 260 265 270
 Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
 275 280 285
 Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser
 290 295 300
 Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala

305	310	315	320
Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu			
325	330	335	
Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr			
340	345	350	
Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg			
355	360	365	
Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr			
370	375	380	
Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser			
385	390	395	400
Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp			
405	410	415	
Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn			
420	425	430	
Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser			
435	440	445	
Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile			
450	455	460	
Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn			
465	470	475	480
Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val			
485	490	495	
Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro			
500	505	510	
Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln			
515	520	525	
Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser			
530	535	540	
Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn			
545	550	555	560
Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser			
565	570	575	
Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly			
580	585	590	
Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly			
595	600	605	

Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln
 610 615 620
 Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
 625 630 635 640
 Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
 645 650 655
 Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile
 660 665 670
 Thr Val Ser Ala Ser Gly Thr Ser Arg Ser Thr Pro Ile Pro Phe Ser
 675 680 685
 Tyr Ser Lys Asn Leu Asp Cys Trp Val Asp Asn Glu Glu Asp Ile Asp
 690 695 700
 Val Ile Leu Lys Lys Ser Thr Ile Leu Asn Leu Asp Ile Asn Asn Asp
 705 710 715 720
 Ile Ile Ser Asp Ile Ser Gly Phe Asn Ser Ser Val Ile Thr Tyr Pro
 725 730 735
 Asp Ala Gln Leu Val Pro Gly Ile Asn Gly Lys Ala Ile His Leu Val
 740 745 750
 Asn Asn Glu Ser Ser Glu Val Ile Val His Lys Ala Met Asp Ile Glu
 755 760 765
 Tyr Asn Asp Met Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val
 770 775 780
 Pro Lys Val Ser Ala Ser His Leu Glu Gln Tyr Gly Thr Asn Glu Tyr
 785 790 795 800
 Ser Ile Ile Ser Ser Met Lys Lys His Ser Leu Ser Ile Gly Ser Gly
 805 810 815
 Trp Ser Val Ser Leu Lys Gly Asn Asn Leu Ile Trp Thr Leu Lys Asp
 820 825 830
 Ser Ala Gly Glu Val Arg Gln Ile Thr Phe Arg Asp Leu Pro Asp Lys
 835 840 845
 Phe Asn Ala Tyr Leu Ala Asn Lys Trp Val Phe Ile Thr Ile Thr Asn
 850 855 860
 Asp Arg Leu Ser Ser Ala Asn Leu Tyr Ile Asn Gly Val Leu Met Gly
 865 870 875 880
 Ser Ala Glu Ile Thr Gly Leu Gly Ala Ile Arg Glu Asp Asn Asn Ile
 885 890 895
 Thr Leu Lys Leu Asp Arg Cys Asn Asn Asn Gln Tyr Val Ser Ile

900	905	910
Asp Lys Phe Arg Ile Phe Cys Lys Ala Leu Asn Pro Lys Glu Ile Glu		
915	920	925
Lys Leu Tyr Thr Ser Tyr Leu Ser Ile Thr Phe Leu Arg Asp Phe Trp		
930	935	940
Gly Asn Pro Leu Arg Tyr Asp Thr		
945	950	

<210> 46

<211> 907

<212> PRT

<213> Artificial Sequence

<220>

<223> CEA-FcIgG fusion

<400> 46

Met	Glu	Ser	Pro	Ser	Ala	Pro	Pro	His	Arg	Trp	Cys	Ile	Pro	Trp	Gln
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Arg	Leu	Leu	Leu	Thr	Ala	Ser	Leu	Leu	Thr	Phe	Trp	Asn	Pro	Pro	Thr
				20				25				30			

Thr	Ala	Lys	Leu	Thr	Ile	Glu	Ser	Thr	Pro	Phe	Asn	Val	Ala	Glu	Gly
		35				40					45				

Lys	Glu	Val	Leu	Leu	Leu	Val	His	Asn	Leu	Pro	Gln	His	Leu	Phe	Gly
		50				55			60						

Tyr	Ser	Trp	Tyr	Lys	Gly	Glu	Arg	Val	Asp	Gly	Asn	Arg	Gln	Ile	Ile
		65				70			75			80			

Gly	Tyr	Val	Ile	Gly	Thr	Gln	Gln	Ala	Thr	Pro	Gly	Pro	Ala	Tyr	Ser
		85				90					95				

Gly	Arg	Glu	Ile	Ile	Tyr	Pro	Asn	Ala	Ser	Leu	Leu	Ile	Gln	Asn	Ile
			100			105				110					

Ile	Gln	Asn	Asp	Thr	Gly	Phe	Tyr	Thr	Leu	His	Val	Ile	Lys	Ser	Asp
			115			120			125						

Leu	Val	Asn	Glu	Glu	Ala	Thr	Gly	Gln	Phe	Arg	Val	Tyr	Pro	Glu	Leu
		130				135			140						

Pro	Lys	Pro	Ser	Ile	Ser	Ser	Asn	Asn	Ser	Lys	Pro	Val	Glu	Asp	Lys
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145	150	155	160
Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr			
165	170	175	
Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln			
180	185	190	
Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn			
195	200	205	
Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg			
210	215	220	
Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro			
225	230	235	240
Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn			
245	250	255	
Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe			
260	265	270	
Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn			
275	280	285	
Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser			
290	295	300	
Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala			
305	310	315	320
Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu			
325	330	335	
Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr			
340	345	350	
Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg			
355	360	365	
Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr			
370	375	380	
Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser			
385	390	395	400
Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp			
405	410	415	
Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn			
420	425	430	
Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser			
435	440	445	

Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
 450 455 460
 Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn
 465 470 475 480
 Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val
 485 490 495
 Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro
 500 505 510
 Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln
 515 520 525
 Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser
 530 535 540
 Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn
 545 550 555 560
 Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser
 565 570 575
 Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly
 580 585 590
 Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly
 595 600 605
 Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln
 610 615 620
 Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
 625 630 635 640
 Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
 645 650 655
 Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile
 660 665 670
 Thr Val Ser Ala Ser Gly Thr Ser Arg Lys Thr His Thr Cys Pro Pro
 675 680 685
 Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
 690 695 700
 Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
 705 710 715 720
 Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
 725 730 735
 Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg

740	745	750
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val		
755	760	765
Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser		
770	775	780
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys		
785	790	795
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp		
805	810	815
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe		
820	825	830
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu		
835	840	845
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe		
850	855	860
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly		
865	870	875
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr		
885	890	895
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<210> 47
 <211> 825
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> N-terminal domain of fragment C of tetanus toxin

<400> 47
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 attatatcag atatatctgg gtttaattca tctgtataaa catatccaga tgctcaattg 180
 gtgcccgaa taaatggcaa agcaatacat ttagtaaaca atgaatcttc tgaagttata 240
 gtgcataaaag ctatggatat tgaatataat gatatgttta ataattttac cgtagcttt 300

tggttgaggg ttcctaaagt atctgctagt cattagaac aatatggcac aaatgagtat 360
 tcaataatta gctctatgaa aaaacatagt ctatcaatag gatctgggtg gagtgtatca 420
 ctaaaggta ataacttaat atggacttta aaagattccg cgggagaagt tagacaaata 480
 acttttaggg atttacctga taaatttaat gcttatttag caaataaaatg gggttttata 540
 actattacta atgatagatt atcttctgct aatttgtata taaatggagt acttatggga 600
 agtgcagaaa ttactggttt aggagctatt agagaggata ataataaac attaaaacta 660
 gatagatgta ataataataa tcaatacggt tctattgata aatttaggat atttgcaaa 720
 gcattaaatc caaaagagat taaaaattta tacacaagtt atttatctat aacctttta 780
 agagacttct gggaaaccc tttacgatat gatacagata ggtag 825

<210> 48

<211> 274

<212> PRT

<213> Artificial Sequence

<220>

<223> N-terminal domain of fragment C of tetanus toxin

<400> 48

Asp	Ser	Thr	Pro	Ile	Pro	Phe	Ser	Tyr	Ser	Lys	Asn	Leu	Asp	Cys	Trp
1															
1															
5															
10															
15															

Val	Asp	Asn	Glu	Glu	Asp	Ile	Asp	Val	Ile	Leu	Lys	Lys	Ser	Thr	Ile
20															
25															
30															

Leu	Asn	Leu	Asp	Ile	Asn	Asn	Asp	Ile	Ile	Ser	Asp	Ile	Ser	Gly	Phe
35															
40															
45															

Asn	Ser	Ser	Val	Ile	Thr	Tyr	Pro	Asp	Ala	Gln	Leu	Val	Pro	Gly	Ile
50															
55															
60															

Asn	Gly	Lys	Ala	Ile	His	Leu	Val	Asn	Asn	Glu	Ser	Ser	Glu	Val	Ile
65															
70															
75															
80															

Val	His	Lys	Ala	Met	Asp	Ile	Glu	Tyr	Asn	Asp	Met	Phe	Asn	Asn	Phe
85															
90															
95															

Thr	Val	Ser	Phe	Trp	Leu	Arg	Val	Pro	Lys	Val	Ser	Ala	Ser	His	Leu
100															
105															
110															

Glu	Gln	Tyr	Gly	Thr	Asn	Glu	Tyr	Ser	Ile	Ile	Ser	Ser	Met	Lys	Lys
115															
120															
125															

His	Ser	Leu	Ser	Ile	Gly	Ser	Gly	Trp	Ser	Val	Ser	Leu	Lys	Gly	Asn
130															
135															
140															

Asn Leu Ile Trp Thr Leu Lys Asp Ser Ala Gly Glu Val Arg Gln Ile
 145 150 155 160
 Thr Phe Arg Asp Leu Pro Asp Lys Phe Asn Ala Tyr Leu Ala Asn Lys
 165 170 175
 Trp Val Phe Ile Thr Ile Thr Asn Asp Arg Leu Ser Ser Ala Asn Leu
 180 185 190
 Tyr Ile Asn Gly Val Leu Met Gly Ser Ala Glu Ile Thr Gly Leu Gly
 195 200 205
 Ala Ile Arg Glu Asp Asn Asn Ile Thr Leu Lys Leu Asp Arg Cys Asn
 210 215 220
 Asn Asn Asn Gln Tyr Val Ser Ile Asp Lys Phe Arg Ile Phe Cys Lys
 225 230 235 240
 Ala Leu Asn Pro Lys Glu Ile Glu Lys Leu Tyr Thr Ser Tyr Leu Ser
 245 250 255
 Ile Thr Phe Leu Arg Asp Phe Trp Gly Asn Pro Leu Arg Tyr Asp Thr
 260 265 270
 Asp Arg

<210> 49
 <211> 2857
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CEA-DOM fusion

<400> 49
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 ggatatgtaa taggaactca acaagctacc ccagggccccg catacagtgg tcgagagata 300
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 accctacacg tcataaaagtc agatcttgtg aatgaagaag caactggcca gttccgggta 420
 tacccggagc tgcccaagcc ctccatctcc agcaacaact ccaaaccgt ggaggacaag 480

gatgctgtgg cttcacctg tgaacctgag actcaggacg caacacct 540
 aacaatcaga gcctcccggt cagtcaggc ctgcagctgt ccaatggcaa caggaccctc 600
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 gcccataact cagacactgg cctcaatagg accacagtca cgacgatcac agtctatgca 960
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gatagatgta ataataataa tcaataacgtt tctattgata aatttaggat attttgcaaa 2760
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 agagacttct gggaaaccc tttacgatat gatatag 2857

<210> 50

<211> 2859

<212> DNA

<213> Artificial Sequence

<220>

<223> rhCEA-DOMopt fusion

<400> 50

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 cggcccttca acgtggccga gggcaaggag gtgctgctgc tggcccacaa cgtgagccag 180
 aacctgttcg gctacatctg gtacaagggc gagcgcgtgg acgcccagccg cccatcgcc 240
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<210> 51
 <211> 952
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> rhCEA-DOMopt fusion

<400> 51
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 Thr Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr

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Thr Ala Gln Leu Thr Ile Glu Ser Arg Pro Phe Asn Val Ala Glu Gly		
35	40	45
Lys Glu Val Leu Leu Ala His Asn Val Ser Gln Asn Leu Phe Gly		
50	55	60
Tyr Ile Trp Tyr Lys Gly Glu Arg Val Asp Ala Ser Arg Arg Ile Gly		
65	70	75
Ser Cys Val Ile Arg Thr Gln Gln Ile Thr Pro Gly Pro Ala His Ser		
85	90	95
Gly Arg Glu Thr Ile Asp Phe Asn Ala Ser Leu Leu Ile His Asn Val		
100	105	110
Thr Gln Ser Asp Thr Gly Ser Tyr Thr Ile Gln Val Ile Lys Glu Asp		
115	120	125
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu		
130	135	140
Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys		
145	150	155
Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr Thr Tyr		
165	170	175
Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Glu		
180	185	190
Leu Ser Ser Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro Arg Asn		
195	200	205
Asp Thr Thr Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Val Arg		
210	215	220
Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro		
225	230	235
Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn Leu Asn		
245	250	255
Leu Thr Cys His Ala Ala Ser Asn Pro Thr Ala Gln Tyr Phe Trp Phe		
260	265	270
Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn		
275	280	285
Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His Asn Ser		
290	295	300
Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val Tyr Ala		
305	310	315
		320

Glu Leu Pro Lys Pro Tyr Ile Thr Ser Asn Asn Ser Asn Pro Ile Glu
 325 330 335
 Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr
 340 345 350
 Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser Ser Arg
 355 360 365
 Leu Glu Leu Ser Asn Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro
 370 375 380
 Arg Asn Asp Thr Thr Phe Tyr Glu Cys Glu Thr Gln Asn Pro Val Ser
 385 390 395 400
 Val Arg Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp
 405 410 415
 Ala Pro Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn
 420 425 430
 Leu Asn Leu Ser Cys His Ala Ala Ser Asn Pro Ala Ala Gln Tyr Ser
 435 440 445
 Trp Phe Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile
 450 455 460
 Pro Asn Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His
 465 470 475 480
 Asn Ser Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val
 485 490 495
 Tyr Val Glu Leu Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro
 500 505 510
 Ile Glu Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Val Ala Glu
 515 520 525
 Asn Thr Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser
 530 535 540
 Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Ile Leu Thr Leu Leu Ser
 545 550 555 560
 Val Thr Arg Asn Asp Thr Gly Pro Tyr Glu Cys Gly Ile Gln Asn Ser
 565 570 575
 Glu Ser Ala Lys Arg Ser Asp Pro Val Thr Leu Asn Val Thr Tyr Gly
 580 585 590
 Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Leu Ser Tyr Arg Ser Gly
 595 600 605
 Ala Asn Leu Asn Leu Ser Cys His Ser Asp Ser Asn Pro Ser Pro Gln

610	615	620
Tyr Ser Trp Leu Ile Asn Gly Thr Leu Arg Gln His Thr Gln Val Leu		
625	630	635
Phe Ile Ser Lys Ile Thr Ser Asn Asn Ser Gly Ala Tyr Ala Cys Phe		
645	650	655
Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Asn Ile		
660	665	670
Ser Val Ser Ser Gly Asp Ser Ser Arg Ser Thr Pro Ile Pro Phe Ser		
675	680	685
Tyr Ser Lys Asn Leu Asp Cys Trp Val Asp Asn Glu Glu Asp Ile Asp		
690	695	700
Val Ile Leu Lys Lys Ser Thr Ile Leu Asn Leu Asp Ile Asn Asn Asp		
705	710	715
Ile Ile Ser Asp Ile Ser Gly Phe Asn Ser Ser Val Ile Thr Tyr Pro		
725	730	735
Asp Ala Gln Leu Val Pro Gly Ile Asn Gly Lys Ala Ile His Leu Val		
740	745	750
Asn Asn Glu Ser Ser Glu Val Ile Val His Lys Ala Met Asp Ile Glu		
755	760	765
Tyr Asn Asp Met Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val		
770	775	780
Pro Lys Val Ser Ala Ser His Leu Glu Gln Tyr Gly Thr Asn Glu Tyr		
785	790	795
Ser Ile Ile Ser Ser Met Lys Lys His Ser Leu Ser Ile Gly Ser Gly		
805	810	815
Trp Ser Val Ser Leu Lys Gly Asn Asn Leu Ile Trp Thr Leu Lys Asp		
820	825	830
Ser Ala Gly Glu Val Arg Gln Ile Thr Phe Arg Asp Leu Pro Asp Lys		
835	840	845
Phe Asn Ala Tyr Leu Ala Asn Lys Trp Val Phe Ile Thr Ile Thr Asn		
850	855	860
Asp Arg Leu Ser Ser Ala Asn Leu Tyr Ile Asn Gly Val Leu Met Gly		
865	870	875
Ser Ala Glu Ile Thr Gly Leu Gly Ala Ile Arg Glu Asp Asn Asn Ile		
885	890	895
Thr Leu Lys Leu Asp Arg Cys Asn Asn Asn Asn Gln Tyr Val Ser Ile		
900	905	910

Asp	Lys	Phe	Arg	Ile	Phe	Cys	Lys	Ala	Leu	Asn	Pro	Lys	Glu	Ile	Glu
915															
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945															
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<210> 52
 <211> 2359
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> rhCEA-CTB_{opt} fusion

<400> 52

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<210> 53

<211> 784

<212> PRT

<213> Artificial Sequence

<220>

<223> rhCEA-CTBopt fusion

<400> 53

Met Gly Ser Pro Ser Ala Pro Leu His Arg Trp Cys Ile Pro Trp Gln

1

5

10

15

Thr Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr

20

25

30

Thr Ala Gln Leu Thr Ile Glu Ser Arg Pro Phe Asn Val Ala Glu Gly

35

40

45

Lys Glu Val Leu Leu Ala His Asn Val Ser Gln Asn Leu Phe Gly

50	55	60
Tyr Ile Trp Tyr Lys Gly Glu Arg Val Asp Ala Ser Arg Arg Ile Gly		
65	70	75
Ser Cys Val Ile Arg Thr Gln Gln Ile Thr Pro Gly Pro Ala His Ser		
85	90	95
Gly Arg Glu Thr Ile Asp Phe Asn Ala Ser Leu Leu Ile His Asn Val		
100	105	110
Thr Gln Ser Asp Thr Gly Ser Tyr Thr Ile Gln Val Ile Lys Glu Asp		
115	120	125
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu		
130	135	140
Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys		
145	150	155
Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr Thr Tyr		
165	170	175
Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Glu		
180	185	190
Leu Ser Ser Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro Arg Asn		
195	200	205
Asp Thr Thr Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Val Arg		
210	215	220
Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro		
225	230	235
Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn Leu Asn		
245	250	255
Leu Thr Cys His Ala Ala Ser Asn Pro Thr Ala Gln Tyr Phe Trp Phe		
260	265	270
Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn		
275	280	285
Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His Asn Ser		
290	295	300
Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val Tyr Ala		
305	310	315
Glu Leu Pro Lys Pro Tyr Ile Thr Ser Asn Asn Ser Asn Pro Ile Glu		
325	330	335
Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr		
340	345	350

Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser Ser Arg
 355 360 365
 Leu Glu Leu Ser Asn Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro
 370 375 380
 Arg Asn Asp Thr Thr Phe Tyr Glu Cys Glu Thr Gln Asn Pro Val Ser
 385 390 395 400
 Val Arg Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp
 405 410 415
 Ala Pro Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn
 420 425 430
 Leu Asn Leu Ser Cys His Ala Ala Ser Asn Pro Ala Ala Gln Tyr Ser
 435 440 445
 Trp Phe Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile
 450 455 460
 Pro Asn Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His
 465 470 475 480
 Asn Ser Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val
 485 490 495
 Tyr Val Glu Leu Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro
 500 505 510
 Ile Glu Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Val Ala Glu
 515 520 525
 Asn Thr Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser
 530 535 540
 Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Ile Leu Thr Leu Leu Ser
 545 550 555 560
 Val Thr Arg Asn Asp Thr Gly Pro Tyr Glu Cys Gly Ile Gln Asn Ser
 565 570 575
 Glu Ser Ala Lys Arg Ser Asp Pro Val Thr Leu Asn Val Thr Tyr Gly
 580 585 590
 Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Leu Ser Tyr Arg Ser Gly
 595 600 605
 Ala Asn Leu Asn Leu Ser Cys His Ser Asp Ser Asn Pro Ser Pro Gln
 610 615 620
 Tyr Ser Trp Leu Ile Asn Gly Thr Leu Arg Gln His Thr Gln Val Leu
 625 630 635 640
 Phe Ile Ser Lys Ile Thr Ser Asn Asn Ser Gly Ala Tyr Ala Cys Phe

645	650	655
Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Asn Ile		
660	665	670
Ser Val Ser Ser Gly Asp Ser Ser Arg Thr Pro Gln Asn Ile Thr Asp		
675	680	685
Leu Cys Ala Glu Tyr His Asn Thr Gln Ile Tyr Thr Leu Asn Asp Lys		
690	695	700
Ile Phe Ser Tyr Thr Glu Ser Leu Ala Gly Lys Arg Glu Met Ala Ile		
705	710	715
Ile Thr Phe Lys Asn Gly Ala Ile Phe Gln Val Glu Val Pro Gly Ser		
725	730	735
Gln His Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr		
740	745	750
Leu Arg Ile Ala Tyr Leu Thr Glu Ala Lys Val Glu Lys Leu Cys Val		
755	760	765
Trp Asn Asn Lys Thr Pro His Ala Ile Ala Ala Ile Ser Met Ala Asn		
770	775	780

<210> 54
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> chemically synthesized

<400> 54
 Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala
 1 5 10 15
 Ser His Leu Glu
 20